

OIKE

RAW SEQUENCE LISTING

DATE: 06/26/2001

PATENT APPLICATION: US/09/836,077

TIME: 07:54:50

Input Set : A:\00015082.app

Output Set: N:\CRF3\06262001\I836077.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: FLECKENSTEIN, Bernhard

7 ENSER, Armin

9 (ii) TITLE OF INVENTION: HUMAN SEMAPHORIN L (H-SEMA) AND

10 CORRESPONDING SEMAPHORINS IN OTHER SPECIES

12 (iii) NUMBER OF SEQUENCES: 44

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Frommer Lawrence & Haug LLP

16 (B) STREET: 745 Fifth Avenue

17 (C) CITY: New York

18 (D) STATE: New York

19 (E) COUNTRY: USA

20 (F) ZIP: 10151

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/836,077

C--> 30 (B) FILING DATE: 16-Apr-2001

31 (C) CLASSIFICATION:

33 (viii) ATTORNEY/AGENT INFORMATION:

34 (A) NAME: Lawrence, William F.

35 (B) REGISTRATION NUMBER: 28,029

36 (C) REFERENCE/DOCKET NUMBER: 514429-3647

38 (ix) TELECOMMUNICATION INFORMATION:

39 (A) TELEPHONE: 212-588-0800

40 (B) TELEFAX: 212-588-0500

43 (2) INFORMATION FOR SEQ ID NO: 1:

45 (i) SEQUENCE CHARACTERISTICS:

46 (A) LENGTH: 2636 base pairs

47 (B) TYPE: nucleic acid

48 (C) STRANDEDNESS: single

49 (D) TOPOLOGY: linear

51 (ii) MOLECULE TYPE: DNA (genomic)

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

58	CGGGGCCACG	GGATGACGCC	TCCTCCGCCC	GGACGTGCCG	CCCCCAGCGC	ACCGCGCGCC	60
60	CGCGTCCCTG	GCCCCCGGCG	TCGGTTGGGG	CTTCCGCTGC	GGCTGCGGCT	GCTGCTGCTG	120
62	CTCTGGGCGG	CCGCCGCCTC	CGCCCAGGGC	CACCTAAGGA	GCGGACCCCG	CATCTTCGCC	180
64	GTCTGGAAG	GCCATGTAGG	GCAGGACCGG	GTGGACTTTG	GCCAGACTGA	GCCGCACACG	240
66	GTGCTTTTCC	ACGAGCCAGG	CAGCTCCTCT	GTGTGGGTGG	GAGGACGTGG	CAAGGTCTAC	300
68	CTCTTTTACT	TCCCCGAGGG	CAAGAACGCA	TCTGTGCGCA	CGGTGAATAT	CGGCTCCACA	360
70	AAGGGGTCCT	GTCTGGATAA	GCGGGACTGC	GAGAACTACA	TCACTCTCCT	GGAGAGGCGG	420
72	AGTGAGGGGC	TGCTGGCCTG	TGGCACCAAC	GCCCCGCACC	CCAGCTGCTG	GAACCTGGTG	480
74	AATGGCACTG	TGGTGCCACT	TGGCGAGATG	AGAGGCTACG	CCCCCTTCAG	CCCGGACGAG	540

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76 AACTCCCTGG TTCTGTTTGA AGGGGACGAG GTGTATTCCA CCATCCGGAA GCAGGAATAC      600
78 AATGGGAAGA TCCCTCGGTT CCGCCGCATC CGGGGCGAGA GTGAGCTGTA CACCAGTGAT      660
80 ACTGTCAATG AGAACCACCA GTTCATCAAA GCCACCATCG TGCACCAAGA CCAGGCTTAC      720
82 GATGACAAGA TCTACTACTT CTTCCGAGAG GACAATCCTG ACAAGAATCC TGAGGCTCCT      780
84 CTCAATGTGT CCCGTGTGGC CCAGTTGTGC AGGGGGGACC AGGGTGGGGA AAGTTCACTG      840
86 TCAGTCTCCA AGTGGAACAC TTTTCTGAAA GCCATGCTGG TATGCAGTGA TGCTGCCACC      900
88 AACAGAAGCT TCAACAGGCT GCAAGACGTC TTCCTGCTCC CTGACCCAG CGGCCAGTGG      960
90 AGGGACACCA GGGTCTATGG TGTTTTCTCC AACCCTGGA ACTACTCAGC CGTCTGTGTG     1020
92 TATTCCTCG GTGACATTGA CAAGGTCTTC CGTACCTCCT CACTCAAGGG CTACCACTCA     1080
94 AGCCTTCCCA ACCCGCGGCC TGGCAAGTGC CTCCAGACC AGCAGCCGAT ACCACAGAG     1140
96 ACCTTCCAGG TGGCTGACCG TCACCCAGAG GTGGCGCAGA GGGTGGAGCC CATGGGGCCT     1200
98 CTGAAGACGC CATTGTCCA CTCTAAATAC CACTACCAGA AAGTGGCCGT TCACCGCATG     1260
100 CAAGCCAGCC ACGGGGAGAC CTTTCATGTG CTTTACCTAA CTACAGACAG GGGCACTATC     1320
102 CACAAGGTGG TGGAACCGGG GGAGCAGGAG CACAGCTTCG CCTTCAACAT CATGGAGATC     1380
104 CAGCCCTTCC GCCGCGCGGC TGCCATCCAG ACCATGTCGC TGGATGCTGA GCGGAGGAAG     1440
106 CTGTATGTGA GCTCCAGTG GGAGGTGAGC CAGGTGCCCC TGGACCTGTG TGAGGTCTAT     1500
108 GCGGGGGGCT GCCACGGTTG CCTCATGTCC CGAGACCCCT ACTGCGGCTG GGACCAGGGC     1560
110 CGCTGCATCT CCATCTACAG CTCCGAACGG TCAGTGCTGC AATCCATTAA TCCAGCCGAG     1620
112 CCACACAAGG AGTGTCCTAA CCCCCAACCA GACAAGGCCC CACTGCAGAA GGTTCCTCTG     1680
114 GCCCCAAACT CTCGCTACTA CTGAGCTGTC CCCATGGAAT CCCGCCACGC CACCTACTCA     1740
116 TGGCGCCACA AGGAGAACGT GGAGCAGAGC TGCGAACCTG GTCACCAGAG CCCCAACTGC     1800
118 ATCCTGTTCA TCGAGAACCT CACGGCGCAG CAGTACGGCC ACTACTTCTG CGAGGCCCAG     1860
120 GAGGGCTCCT ACTTCCGCGA GGCTCAGCAC TGGCAGCTGC TGCCCGAGGA CGGCATCATG     1920
122 GCCGAGCACC TGCTGGGTCA TGCCTGTGCC CTGGCTGCCT CCCTCTGGCT GGGGGTGCTG     1980
124 CCCACACTCA CTCTTGCTT GCTGGTCCAC TAGGGCCTCC CGAGGCTGGG CATGCCTCAG     2040
126 GCTTCTGCAG CCCAGGGCAC TAGAACGTCT CACACTCAGA GCCGGCTGGC CCGGGAGCTC     2100
128 CTTGCCTGCC ACTTCTTCCA GGGGACAGAA TAACCCAGTG GAGGATGCCA GGCCTGGAGA     2160
130 CGTCCAGCCG CAGGCGGCTG CTGGGCCCCA GGTGGCGCAC GGATGGTGAG GGGCTGAGAA     2220
132 TGAGGGCACC GACTGTGAAG CTGGGGCATC GATGACCCAA GACTTTATCT TCTGGAATAAT     2280
134 ATTTTTCAGA CTCTCAAAC TTGACTAAAT GCAGCGATGC TCCCAGCCCA AGAGCCCATG     2340
136 GGTCGGGGAG TGGGTTTGGA TAGGAGAGCT GGGACTCCAT CTCGACCCTG GGGCTGAGGC     2400
138 CTGAGTCCTT CTGGACTCTT GGTACCCACA TTGCCTCCTT CCCCTCCCTC TCTCATGGCT     2460
140 GGGTGGCTGG GTTTCCTGAA GACCCAGGGC TACCCTCTGT CCAGCCCTGT CCTCTGCAGC     2520
142 TCCCTCTCTG GTCCTGGGTC CCACAGGACA GCCGCCTTGC ATGTTTATTG AAGGATGTTT     2580
144 GCTTCCGGA CGGAAGGACG GAAAAAGCTC TGAAAAAAAA AAAAAAAAAA AAAAAA     2636
146 (2) INFORMATION FOR SEQ ID NO: 2:
148 (i) SEQUENCE CHARACTERISTICS:
149 (A) LENGTH: 1195 base pairs
150 (B) TYPE: nucleic acid
151 (C) STRANDEDNESS: single
152 (D) TOPOLOGY: linear
154 (ii) MOLECULE TYPE: DNA (genomic)
159 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
161 CGGGGCTGCG GGATGACGCC TCCTCCTCCC GGACGTGCCG CCCCAGCGC ACCGCGCGCC      60
163 CGCGTCCTCA GCCTGCCGGC TCGGTTCTGGG CTCCCCTGTC GGCTGCGGCT TCTGCTGGTG     120
165 TTCTGGGTGG CCGCCGCCTC CGCCCAAGGC CACTCGAGGA GCGGACCCCG CATCTCCGCC     180
167 GTCTGGAAG GGCAGGACCA TGTGGACTTT AGCCAGCCTG AGCCACACAC CGTGCTTTTC     240
169 CATGAGCCGG GCAGCTTCTC TGTCTGGGTG GGTGGACGTG GCAAGGTCTA CCACTTCAAC     300
171 TTCCCCGAGG GCAAGAATGC CTCTGTGCGC ACGGTGAACA TCGGCTCCAC AAAGGGGTCC     360

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173 TGTCAGGACA AACAGGACTG TGGGAATTAC ATCACTCTTC TAGAAAGGCG GGGTAATGGG      420
175 CTGCTGGTCT GTGGCACCAA TGCCCGGAAG CCCAGCTGCT GGAAGTTGGT GAATGACAGT      480
177 GTGGTGATGT CACTTGGTGA GATGAAAGGC TATGCCCCCT TCAGCCCGGA TGAGAACTCC      540
179 CTGGTTCTGT TTGAAGGAGA TGAAGTGTA TCTACCATCC GGAAGCAGGA ATACAACGGG      600
181 AAGATCCCTC GGTTCGACG CATTCGGGGC GAGAGTGAAC TGTACACAAG TGATACAGTC      660
183 ATGCAGAACC CACAGTTCAT CAAGGCCACC ATTGTGCACC AAGACCAAGC CTATGATGAT      720
185 AAGATCTACT ACTTCTCCG AGAAGACAAC CCTGACAAGA ACCCCGAGGC TCCTCTCAAT      780
187 GTGTCCCAG TAGCCAGTT GTGCAGGGGG GACCAGGGTG GTGAGAGTTC GTTGTCTGTC      840
189 TCCAAGTGA ACACCTTCCT GAAAGCCATG TTGGTCTGCA GCGATGCAGC CACCAACAGG      900
191 AACTTCAATC GGCTGCAAGA TGTCTTCTG CTCCCTGACC CCAGTGGCCA GTGGAGAGAT      960
193 ACCAGGTCT ATGGCGTTT CTCCAACCCC TGGAACTACT CAGCTGTCTG CGTGTATTCTG     1020
195 CTTGGTGACA TTGACAGAGT CTTCCGTACC TCATCGCTCA AAGGCTACCA CATGGGCCTT     1080
197 TCCAACCTC GACCTGGCAT GTGCCTCCCA AAAAAGCAGC CCATACCCAC AGAAACCTTC     1140
199 CAGGTAGCTG ATAGTCACCC AGAGGTGGCT CAGAGGGTGG AACCTATGGG GCCCC      1195

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201 (2) INFORMATION FOR SEQ ID NO: 3:

203 (i) SEQUENCE CHARACTERISTICS:

204 (A) LENGTH: 666 amino acids

205 (B) TYPE: amino acid

W--> 206 (C) STRANDEDNESS: n/a

207 (D) TOPOLOGY: linear

W--> 209 (ii) MOLECULE TYPE: amino acid

214 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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216 Met Thr Pro Pro Pro Pro Gly Arg Ala Ala Pro Ser Ala Pro Arg Ala
217 1 5 10 15
219 Arg Val Pro Gly Pro Pro Ala Arg Leu Gly Leu Pro Leu Arg Leu Arg
220 20 25 30
222 Leu Leu Leu Leu Leu Trp Ala Ala Ala Ala Ser Ala Gln Gly His Leu
223 35 40 45
225 Arg Ser Gly Pro Arg Ile Phe Ala Val Trp Lys Gly His Val Gly Gln
226 50 55 60
228 Asp Arg Val Asp Phe Gly Gln Thr Glu Pro His Thr Val Leu Phe His
229 65 70 75 80
231 Glu Pro Gly Ser Ser Ser Val Trp Val Gly Gly Arg Gly Lys Val Tyr
232 85 90 95
234 Leu Phe Asp Phe Pro Glu Gly Lys Asn Ala Ser Val Arg Thr Val Asn
235 100 105 110
237 Ile Gly Ser Thr Lys Gly Ser Cys Leu Asp Lys Arg Asp Cys Glu Asn
238 115 120 125
240 Tyr Ile Thr Leu Leu Glu Arg Arg Ser Glu Gly Leu Leu Ala Cys Gly
241 130 135 140
243 Thr Asn Ala Arg His Pro Ser Cys Trp Asn Leu Val Asn Gly Thr Val
244 145 150 155 160
246 Val Pro Leu Gly Glu Met Arg Gly Tyr Ala Pro Phe Ser Pro Asp Glu
247 165 170 175
249 Asn Ser Leu Val Leu Phe Glu Gly Asp Glu Val Tyr Ser Thr Ile Arg
250 180 185 190
252 Lys Gln Glu Tyr Asn Gly Lys Ile Pro Arg Phe Arg Arg Ile Arg Gly
253 195 200 205
255 Glu Ser Glu Leu Tyr Thr Ser Asp Thr Val Met Gln Asn Pro Gln Phe

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256          210          215          220
258   Ile Lys Ala Thr Ile Val His Gln Asp Gln Ala Tyr Asp Asp Lys Ile
259   225          230          235          240
261   Tyr Tyr Phe Phe Arg Glu Asp Asn Pro Asp Lys Asn Pro Glu Ala Pro
262          245          250          255
264   Leu Asn Val Ser Arg Val Ala Gln Leu Cys Arg Gly Asp Gln Gly Gly
265          260          265          270
267   Glu Ser Ser Leu Ser Val Ser Lys Trp Asn Thr Phe Leu Lys Ala Met
268          275          280          285
270   Leu Val Cys Ser Asp Ala Ala Thr Asn Lys Asn Phe Asn Arg Leu Gln
271          290          295          300
273   Asp Val Phe Leu Leu Pro Asp Pro Ser Gly Gln Trp Arg Asp Thr Arg
274   305          310          315          320
276   Val Tyr Gly Val Phe Ser Asn Pro Trp Asn Tyr Ser Ala Val Cys Val
277          325          330          335
279   Tyr Ser Leu Gly Asp Ile Asp Lys Val Phe Arg Thr Ser Ser Leu Lys
280          340          345          350
282   Gly Tyr His Ser Ser Leu Pro Asn Pro Arg Pro Gly Lys Cys Leu Pro
283          355          360          365
285   Asp Gln Gln Pro Ile Pro Thr Glu Thr Phe Gln Val Ala Asp Arg His
286   370          375          380
288   Pro Glu Val Ala Gln Arg Val Glu Pro Met Gly Pro Leu Lys Thr Pro
289   385          390          395          400
291   Leu Phe His Ser Lys Tyr His Tyr Gln Lys Val Ala Val His Arg Met
292          405          410          415
294   Gln Ala Ser His Gly Glu Thr Phe His Val Leu Tyr Leu Thr Thr Asp
295          420          425          430
297   Arg Gly Thr Ile His Lys Val Val Glu Pro Gly Glu Gln Glu His Ser
298          435          440          445
300   Phe Ala Phe Asn Ile Met Glu Ile Gln Pro Phe Arg Arg Ala Ala Ala
301          450          455          460
303   Ile Gln Thr Met Ser Leu Asp Ala Glu Arg Arg Lys Leu Tyr Val Ser
304   465          470          475          480
306   Ser Gln Trp Glu Val Ser Gln Val Pro Leu Asp Leu Cys Glu Val Tyr
307          485          490          495
309   Gly Gly Gly Cys His Gly Cys Leu Met Ser Arg Asp Pro Tyr Cys Gly
310          500          505          510
312   Trp Asp Gln Gly Arg Cys Ile Ser Ile Tyr Ser Ser Glu Arg Ser Val
313          515          520          525
315   Leu Gln Ser Ile Asn Pro Ala Glu Pro His Lys Glu Cys Pro Asn Pro
316          530          535          540
318   Lys Pro Asp Lys Ala Pro Leu Gln Lys Val Ser Leu Ala Pro Asn Ser
319   545          550          555          560
321   Arg Tyr Tyr Leu Ser Cys Pro Met Glu Ser Arg His Ala Thr Tyr Ser
322          565          570          575
324   Trp Arg His Lys Glu Asn Val Glu Gln Ser Cys Glu Pro Gly His Gln
325          580          585          590
327   Ser Pro Asn Cys Ile Leu Phe Ile Glu Asn Leu Thr Ala Gln Gln Tyr
328          595          600          605

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330      Gly His Tyr Phe Cys Glu Ala Gln Glu Gly Ser Tyr Phe Arg Glu Ala
331          610                      615                      620
333      Gln His Trp Gln Leu Leu Pro Glu Asp Gly Ile Met Ala Glu His Leu
334          625                      630                      635                      640
336      Leu Gly His Ala Cys Ala Leu Ala Ala Ser Leu Trp Leu Gly Val Leu
337                      645                      650                      655
339      Pro Thr Leu Thr Leu Gly Leu Leu Val His
340          660                      665
342 (2) INFORMATION FOR SEQ ID NO: 4:
344      (i) SEQUENCE CHARACTERISTICS:
345          (A) LENGTH: 394 amino acids
346          (B) TYPE: amino acid
W--> 347          (C) STRANDEDNESS: n/a
348          (D) TOPOLOGY: linear
W--> 350      (ii) MOLECULE TYPE: amino acid
355      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
357      Met Thr Pro Pro Pro Pro Gly Arg Ala Ala Pro Ser Ala Pro Arg Ala
358          1          5          10          15
360      Arg Val Leu Ser Leu Pro Ala Arg Phe Gly Leu Pro Leu Arg Leu Arg
361          20          25          30
363      Leu Leu Leu Val Phe Trp Val Ala Ala Ala Ser Ala Gln Gly His Ser
364          35          40          45
366      Arg Ser Gly Pro Arg Ile Ser Ala Val Trp Lys Gly Gln Asp His Val
367          50          55          60
369      Asp Phe Ser Gln Pro Glu Pro His Thr Val Leu Phe His Glu Pro Gly
370          65          70          75          80
372      Ser Phe Ser Val Trp Val Gly Gly Arg Gly Lys Val Tyr His Phe Asn
373          85          90          95
375      Phe Pro Glu Gly Lys Asn Ala Ser Val Arg Thr Val Asn Ile Gly Ser
376          100         105         110
378      Thr Lys Gly Ser Cys Gln Asp Lys Gln Asp Cys Gly Asn Tyr Ile Thr
379          115         120         125
381      Leu Leu Glu Arg Arg Gly Asn Gly Leu Leu Val Cys Gly Thr Asn Ala
382          130         135         140
384      Arg Lys Pro Ser Cys Trp Asn Leu Val Asn Asp Ser Val Val Met Ser
385          145         150         155         160
387      Leu Gly Glu Met Lys Gly Tyr Ala Pro Phe Ser Pro Asp Glu Asn Ser
388          165         170         175
390      Leu Val Leu Phe Glu Gly Asp Glu Val Tyr Ser Thr Ile Arg Lys Gln
391          180         185         190
393      Glu Tyr Asn Gly Lys Ile Pro Arg Phe Arg Arg Ile Arg Gly Glu Ser
394          195         200         205
396      Glu Leu Tyr Thr Ser Asp Thr Val Met Gln Asn Pro Gln Phe Ile Lys
397          210         215         220
399      Ala Thr Ile Val His Gln Asp Gln Ala Tyr Asp Asp Lys Ile Tyr Tyr
400          225         230         235         240
402      Phe Phe Arg Glu Asp Asn Pro Asp Lys Asn Pro Glu Ala Pro Leu Asn
403          245         250         255
405      Val Ser Arg Val Ala Gln Leu Cys Arg Gly Asp Gln Gly Gly Glu Ser

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VERIFICATION SUMMARY

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Input Set : A:\00015082.app

Output Set: N:\CRF3\06262001\I836077.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:206 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=3
L:209 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:347 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=4
L:350 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4